## Jade Forwood

List of Publications by Year in descending order

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116	3,306	29	53
papers	citations	h-index	g-index
119	119	119	4280
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Molecular basis for specificity of nuclear import and prediction of nuclear localization. Biochimica Et Biophysica Acta - Molecular Cell Research, 2011, 1813, 1562-1577.	1.9	336
2	Structural Biology and Regulation of Protein Import into the Nucleus. Journal of Molecular Biology, 2016, 428, 2060-2090.	2.0	204
3	Defective importin  recognition and nuclear import of the sex-determining factor SRY are associated with XY sex-reversing mutations. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7045-7050.	3.3	143
4	Crystal Structures of Flax Rust Avirulence Proteins AvrL567-A and -D Reveal Details of the Structural Basis for Flax Disease Resistance Specificity. Plant Cell, 2007, 19, 2898-2912.	3.1	143
5	Functional and structural properties of mammalian acyl-coenzyme A thioesterases. Progress in Lipid Research, 2010, 49, 366-377.	5.3	128
6	The C-terminal 50 Amino Acid Residues of Dengue NS3 Protein Are Important for NS3-NS5 Interaction and Viral Replication. Journal of Biological Chemistry, 2015, 290, 2379-2394.	1.6	105
7	The C-terminal Nuclear Localization Signal of the Sex-determining Region Y (SRY) High Mobility Group Domain Mediates Nuclear Import through Importin $\hat{I}^21$ . Journal of Biological Chemistry, 2001, 276, 46575-46582.	1.6	104
8	Structural Basis of Highâ€Affinity Nuclear Localization Signal Interactions with Importinâ€Î±. Traffic, 2012, 13, 532-548.	1.3	91
9	Nuclear Import of Creb and AP-1 Transcription Factors Requires Importin- $\hat{l}^21$ and Ran but Is Independent of Importin- $\hat{l}_{\pm}$ . Biochemistry, 2001, 40, 5208-5217.	1.2	89
10	Quantitative Structural Analysis of Importin- $\hat{l}^2$ Flexibility: Paradigm for Solenoid Protein Structures. Structure, 2010, 18, 1171-1183.	1.6	89
11	Substrate specificity of protein kinases and computational prediction of substrates. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2005, 1754, 200-209.	1.1	88
12	The 37-Amino-Acid Interdomain of Dengue Virus NS5 Protein Contains a Functional NLS and Inhibitory CK2 Site. Biochemical and Biophysical Research Communications, 1999, 257, 731-737.	1.0	87
13	Structural basis for recruitment of tandem hotdog domains in acyl-CoA thioesterase 7 and its role in inflammation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 10382-10387.	3.3	71
14	The C-terminal 18 Amino Acid Region of Dengue Virus NS5 Regulates its Subcellular Localization and Contains a Conserved Arginine Residue Essential for Infectious Virus Production. PLoS Pathogens, 2016, 12, e1005886.	2.1	66
15	Crystallography and protein–protein interactions: biological interfaces and crystal contacts. Biochemical Society Transactions, 2008, 36, 1438-1441.	1.6	61
16	Lysine-Specific Histone Demethylase 1A Regulates Macrophage Polarization and Checkpoint Molecules in the Tumor Microenvironment of Triple-Negative Breast Cancer. Frontiers in Immunology, 2019, 10, 1351.	2.2	60
17	Phylogeny of beak and feather disease virus in cockatoos demonstrates host generalism and multiple-variant infections within Psittaciformes. Virology, 2014, 460-461, 72-82.	1.1	55
18	Mutability Dynamics of an Emergent Single Stranded DNA Virus in a Na $\tilde{\mathbb{A}}$ -ve Host. PLoS ONE, 2014, 9, e85370.	1.1	54

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19	Structural basis for importin alpha 3 specificity of $W$ proteins in Hendra and Nipah viruses. Nature Communications, 2018, 9, 3703.	5.8	50
20	Targeting Nuclear LSD1 to Reprogram Cancer Cells and Reinvigorate Exhausted T Cells via a Novel LSD1-EOMES Switch. Frontiers in Immunology, 2020, 11, 1228.	2.2	49
21	Evidence of a deep viral host switch event with beak and feather disease virus infection in rainbow bee-eaters (Merops ornatus). Scientific Reports, 2015, 5, 14511.	1.6	45
22	Structural insights into the assembly and regulation of distinct viral capsid complexes. Nature Communications, 2016, 7, 13014.	5.8	43
23	Nuclear Import Pathway of the Telomere Elongation Supressor TRF1: Inhibition by Importin α. Biochemistry, 2002, 41, 9333-9340.	1.2	42
24	Nuclear import inhibitor N -(4-hydroxyphenyl) retinamide targets Zika virus (ZIKV) nonstructural protein 5 to inhibit ZIKV infection. Biochemical and Biophysical Research Communications, 2017, 493, 1555-1559.	1.0	41
25	Calmodulin-dependent nuclear import of HMG-box family nuclear factors: importance of the role of SRY in sex reversal. Biochemical Journal, 2010, 430, 39-48.	1.7	38
26	A novel pathogenic aviadenovirus from red-bellied parrots (Poicephalus rufiventris) unveils deep recombination events among avian host lineages. Virology, 2017, 502, 188-197.	1.1	34
27	Zika Virus NS5 Forms Supramolecular Nuclear Bodies That Sequester Importin-α and Modulate the Host Immune and Pro-Inflammatory Response in Neuronal Cells. ACS Infectious Diseases, 2019, 5, 932-948.	1.8	34
28	Forensic genetic evidence of beak and feather disease virus infection in a Powerful Owl, <i>Ninox strenua</i> . Emu, 2016, 116, 71-74.	0.2	33
29	Kap95p Binding Induces the Switch Loops of RanGDP to Adopt the GTP-Bound Conformation: Implications for Nuclear Import Complex Assembly Dynamics. Journal of Molecular Biology, 2008, 383, 772-782.	2.0	32
30	Novel Flavivirus Antiviral That Targets the Host Nuclear Transport Importin $\hat{l}\pm\hat{l}^21$ Heterodimer. Cells, 2019, 8, 281.	1.8	31
31	Evaluating protein:protein complex formation using synchrotron radiation circular dichroism spectroscopy. Proteins: Structure, Function and Bioinformatics, 2008, 70, 1142-1146.	1.5	28
32	Importin-β Is a GDP-to-GTP Exchange Factor of Ran. Journal of Biological Chemistry, 2009, 284, 22549-22558.	1.6	27
33	Molecular and microscopic characterization of a novel Eastern grey kangaroopox virus genome directly from a clinical sample. Scientific Reports, 2017, 7, 16472.	1.6	26
34	Protein complexes including PGRMC1 and actin-associated proteins are disrupted by AG-205. Biochemical and Biophysical Research Communications, 2020, 524, 64-69.	1.0	26
35	Molecular characterisation of a novel pathogenic avipoxvirus from the Australian magpie (Gymnorhina tibicen). Virology, 2020, 540, 1-16.	1.1	24
36	Structural basis for nuclear import selectivity of pioneer transcription factor SOX2. Nature Communications, 2021, 12, 28.	5.8	24

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37	Structural Characterisation of the Nuclear Import Receptor Importin Alpha in Complex with the Bipartite NLS of Prp20. PLoS ONE, 2013, 8, e82038.	1.1	22
38	Structural Basis for Regulation of the Human Acetyl-CoA Thioesterase 12 and Interactions with the Steroidogenic Acute Regulatory Protein-related Lipid Transfer (START) Domain. Journal of Biological Chemistry, 2014, 289, 24263-24274.	1.6	22
39	Evolution of circoviruses in lorikeets lags behind its hosts. Molecular Phylogenetics and Evolution, 2016, 100, 281-291.	1.2	22
40	Contribution of the residue at position 4 within classical nuclear localization signals to modulating interaction with importins and nuclear targeting. Biochimica Et Biophysica Acta - Molecular Cell Research, 2018, 1865, 1114-1129.	1.9	22
41	Structural Basis for Importin-α Binding of the Human Immunodeficiency Virus Tat. Scientific Reports, 2017, 7, 1650.	1.6	21
42	Beak and feather disease virus genotypes in <scp>Australian</scp> parrots reveal flexible hostâ€switching. Australian Veterinary Journal, 2015, 93, 471-475.	0.5	20
43	Modelling the structure of latexin–carboxypeptidase A complex based on chemical cross-linking and molecular docking. Protein Engineering, Design and Selection, 2006, 19, 9-16.	1.0	19
44	Structural Characterisation of the Beta-Ketoacyl-Acyl Carrier Protein Synthases, FabF and FabH, of Yersinia pestis. Scientific Reports, 2015, 5, 14797.	1.6	19
45	Altered mitogenâ€activated protein kinase signaling in dystrophic ( <i>mdx</i> ) muscle. Muscle and Nerve, 2012, 46, 374-383.	1.0	18
46	Genomic Characterisation of a Highly Divergent Siadenovirus (Psittacine Siadenovirus F) from the Critically Endangered Orange-Bellied Parrot (Neophema chrysogaster). Viruses, 2021, 13, 1714.	1.5	18
47	Protein Structure Determination Using a Combination of Cross-linking, Mass Spectrometry, and Molecular Modeling. Methods in Molecular Biology, 2008, 426, 459-474.	0.4	18
48	Whole-Genome Sequences of Two Beak and Feather Disease Viruses in the Endangered Swift Parrot () Tj ETQq0	0 OrgBT /	Overlock 10 T
49	Structure, function, and regulation of thioesterases. Progress in Lipid Research, 2020, 79, 101036.	5.3	16
50	Characterization of the Complete Genome Sequence of a Beak and Feather Disease Virus from a Moluccan Red Lory ( <i>Eos bornea</i> ). Genome Announcements, 2013, 1, .	0.8	15
51	Functional disruption of yeast metacaspase, Mca1, leads to miltefosine resistance and inability to mediate miltefosine-induced apoptotic effects. Fungal Genetics and Biology, 2014, 67, 71-81.	0.9	15
52	Structural Characterisation of FabG from Yersinia pestis, a Key Component of Bacterial Fatty Acid Synthesis. PLoS ONE, 2015, 10, e0141543.	1.1	15
53	Henipavirus W Proteins Interact with $14\text{-}3\text{-}3$ To Modulate Host Gene Expression. Journal of Virology, 2020, 94, .	1.5	15
54	Focusing in on structural genomics: The University of Queensland structural biology pipeline. New Biotechnology, 2006, 23, 281-289.	2.7	14

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55	The use of Co2+for crystallization and structure determination, using a conventional monochromatic X-ray source, of flax rust avirulence protein. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 209-213.	0.7	14
56	Differential expression of two isolates of beak and feather disease virus capsid protein in Escherichia coli. Journal of Virological Methods, 2013, 189, 118-124.	1.0	14
57	Structural determination of importin alpha in complex with beak and feather disease virus capsid nuclear localization signal. Biochemical and Biophysical Research Communications, 2013, 438, 680-685.	1.0	13
58	Quantitative analysis of DNA-protein interactions using double-labeled native gel electrophoresis and fluorescence-based imaging. Electrophoresis, 2006, 27, 3166-3170.	1.3	12
59	Structural Characterization of a Gcn5-Related N-Acetyltransferase from Staphylococcus aureus. PLoS ONE, 2014, 9, e102348.	1.1	12
60	Rapid genotyping of beak and feather disease virus using high-resolution DNA melt curve analysis. Journal of Virological Methods, 2014, 208, 47-55.	1.0	12
61	Pigeon circoviruses from feral pigeons in Australia demonstrate extensive recombination and genetic admixture with other circoviruses. Avian Pathology, 2019, 48, 512-520.	0.8	12
62	Molecular Characterisation of a Novel and Highly Divergent Passerine Adenovirus 1. Viruses, 2020, 12, 1036.	1.5	12
63	The Intrinsically Disordered W Protein Is Multifunctional during Henipavirus Infection, Disrupting Host Signalling Pathways and Nuclear Import. Cells, 2020, 9, 1913.	1.8	12
64	Ligand-induced Conformational Changes within a Hexameric Acyl-CoA Thioesterase. Journal of Biological Chemistry, 2011, 286, 35643-35649.	1.6	11
65	Human importin $\hat{l}\pm 3$ and its N-terminal truncated form, without the importin- $\hat{l}^2$ -binding domain, are oligomeric species with a low conformational stability in solution. Biochimica Et Biophysica Acta - General Subjects, 2020, 1864, 129609.	1.1	11
66	Targeting novel LSD1-dependent ACE2 demethylation domains inhibits SARS-CoV-2 replication. Cell Discovery, 2021, 7, 37.	3.1	11
67	An efficient approach for recombinant expression and purification of the viral capsid protein from beak and feather disease virus (BFDV) in Escherichia coli. Journal of Virological Methods, 2015, 215-216, 1-8.	1.0	10
68	The first complete mitogenome of Indian ringneck <i>(Psittacula krameri)</i> demonstrates close phylogenetic relationship with Eclectus parrot. Mitochondrial DNA Part B: Resources, 2019, 4, 3579-3581.	0.2	10
69	MERS-CoV ORF4b employs an unusual binding mechanism to target IMPÎ $\pm$ and block innate immunity. Nature Communications, 2022, 13, 1604.	5.8	10
70	A comparison of PCR assays for beak and feather disease virus and high resolution melt (HRM) curve analysis of replicase associated protein and capsid genes. Journal of Virological Methods, 2016, 237, 47-57.	1.0	9
71	Structural insights into GDP-mediated regulation of a bacterial acyl-CoA thioesterase. Journal of Biological Chemistry, 2017, 292, 20461-20471.	1.6	9
72	REPEAT SPILLOVER OF BEAK AND FEATHER DISEASE VIRUS INTO AN ENDANGERED PARROT HIGHLIGHTS THE RISK ASSOCIATED WITH ENDEMIC PATHOGEN LOSS IN ENDANGERED SPECIES. Journal of Wildlife Diseases, 2020, 56, 896-906.	0.3	9

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73	Structural Perspectives of Beak and Feather Disease Virus and Porcine Circovirus Proteins. Viral Immunology, 2021, 34, 49-59.	0.6	9
74	Structural characterization of a GNAT family acetyltransferase from Elizabethkingia anophelis bound to acetyl-CoA reveals a new dimeric interface. Scientific Reports, 2021, 11, 1274.	1.6	9
75	Insights into Acinetobacter baumannii fatty acid synthesis 3-oxoacyl-ACP reductases. Scientific Reports, 2021, 11, 7050.	1.6	9
76	Molecular Characterization of Genome Sequences of Beak and Feather Disease Virus from the Australian Twenty-Eight Parrot ( <i> Barnardius zonarius semitorquatus &lt; /i &gt; ). Genome Announcements, 2014, 2, .</i>	0.8	8
77	Structural and functional characterization of TesB fromYersinia pestisreveals a unique octameric arrangement of hotdog domains. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 986-995.	2.5	8
78	Whole-Genome Sequence Characterization of a Beak and Feather Disease Virus in a Wild Regent Parrot ( Polytelis anthopeplus monarchoides ). Genome Announcements, 2014, 2, .	0.8	7
79	Characterization of a beta-catenin nuclear localization defect in MCF-7 breast cancer cells. Experimental Cell Research, 2016, 341, 196-206.	1.2	7
80	Homology Modelling and Structural Comparisons of Capsid-Associated Proteins from Circoviruses Reveal Important Virus-Specific Surface Antigens. Crystal Structure Theory and Applications, 2012, 01, 9-16.	0.3	7
81	A conserved arginine in NS5 binds genomic $3\hat{a}\in^2$ stem $\hat{a}\in^*$ loop RNA for primer-independent initiation of flavivirus RNA replication. Rna, 2022, 28, 177-193.	1.6	7
82	Crystallization of the C-terminal domain of the mouse brain cytosolic long-chain acyl-CoA thioesterase. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 133-135.	0.7	6
83	Characterization of the Whole-Genome Sequence of a Beak and Feather Disease Virus Isolate from a Mallee Ringneck Parrot (Barnardius zonarius barnardi). Genome Announcements, 2014, 2, .	0.8	6
84	Structural and Functional Characterization of the Paal Thioesterase from Streptococcus pneumoniae Reveals a Dual Specificity for Phenylacetyl-CoA and Medium-chain Fatty Acyl-CoAs and a Novel CoA-induced Fit Mechanism. Journal of Biological Chemistry, 2016, 291, 1866-1876.	1.6	6
85	Characterization of the first mitochondrial genome of a little Corella (Cacatua sanguinea) and its phylogenetic implications. Mitochondrial DNA Part B: Resources, 2019, 4, 3792-3794.	0.2	6
86	The complete mitochondrial genome sequence of an Endangered powerful owl (Ninox strenua). Mitochondrial DNA Part B: Resources, 2016, 1, 722-723.	0.2	5
87	Structural characterisation of the fatty acid biosynthesis enzyme FabF from the pathogen Listeria monocytogenes. Scientific Reports, 2017, 7, 39277.	1.6	5
88	Structural characterization of a short-chain dehydrogenase/reductase from multi-drug resistant Acinetobacter baumannii. Biochemical and Biophysical Research Communications, 2019, 518, 465-471.	1.0	5
89	Assessing circovirus gene flow in multiple spill-over events. Virus Genes, 2019, 55, 802-814.	0.7	5
90	SpeG polyamine acetyltransferase enzyme from Bacillus thuringiensis forms a dodecameric structure and exhibits high catalytic efficiency. Journal of Structural Biology, 2020, 210, 107506.	1.3	5

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91	The Structural Features of Henipavirus Matrix Protein Driving Intracellular Trafficking. Viral Immunology, 2021, 34, 27-40.	0.6	5
92	Nuclear Import Properties of the Sex-Determining Factor SRY., 2007, 390, 83-97.		5
93	Expression, purification and crystallization of acetyl-CoA hydrolase from <i>Neisseria meningitidis</i> . Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 1303-1306.	0.7	4
94	Crystallization and preliminary X-ray diffraction analysis of FabG fromYersinia pestis. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 101-104.	0.4	4
95	Structural characterization of a Type B chloramphenicol acetyltransferase from the emerging pathogen Elizabethkingia anophelis NUHP1. Scientific Reports, 2021, 11, 9453.	1.6	4
96	Crystallization of the flexible nuclear import receptor importin- $\hat{l}^2$ in the unliganded state. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 625-628.	0.7	3
97	Mycobacteria Encode Active and Inactive Classes of TesB Fatty-Acyl CoA Thioesterases Revealed through Structural and Functional Analysis. Biochemistry, 2017, 56, 1460-1472.	1.2	3
98	Structural characterization of βâ€ketoacyl ACP synthase I bound to platencin and fragment screening molecules at two substrate binding sites. Proteins: Structure, Function and Bioinformatics, 2020, 88, 47-56.	1.5	3
99	Structural characterization of the porcine adenoâ€associated virus Po1 capsid protein binding to the nuclear trafficking protein importin alpha. FEBS Letters, 2021, 595, 2793-2804.	1.3	3
100	Selective Targeting of Protein Kinase C (PKC)- $\hat{l}_{s}$ , Nuclear Translocation Reduces Mesenchymal Gene Signatures and Reinvigorates Dysfunctional CD8+ T Cells in Immunotherapy-Resistant and Metastatic Cancers. Cancers, 2022, 14, 1596.	1.7	3
101	Beak and feather disease virus: biology and resultant disease. WikiJournal of Science, 2020, 3, 7.	0.1	2
102	Interaction between Plate Make and Protein in Protein Crystallisation Screening. PLoS ONE, 2009, 4, e7851.	1.1	2
103	Crystallization of the acyl-CoA thioesterase TesB fromYersinia pestis. Acta Crystallographica Section F: Structural Biology Communications, 2013, 69, 188-190.	0.7	1
104	Expression, purification, crystallization and preliminary X-ray analysis of the Paal-like thioesterase SAV0944 fromStaphylococcus aureus. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 244-247.	0.4	1
105	Characterization of Beak and Feather Disease Virus Genomes from Wild Musk Lorikeets ( Glossopsitta) Tj ETQq1	1 8.78431	.4 rgBT /Over
106	Whole-Genome Sequence of a Beak and Feather Disease Virus Isolate from a Fledgling Red-Capped Parrot ( $\mbox{Purpure}$ icephalus spurius $\mbox{< i>}$ ). Genome Announcements, 2016, 4, .	0.8	1
107	The first complete mitogenome of red-bellied parrot (Poicephalus rufiventris) resolves phylogenetic status within Psittacidae. Mitochondrial DNA Part B: Resources, 2018, 3, 195-197.	0.2	1

The first complete mitogenome of Australia's largest raptor, the wedge-tailed eagle (<i>Aquila) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50

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109	Structural basis for disulphide-CoA inhibition of a butyryl-CoA hexameric thioesterase. Journal of Structural Biology, 2020, 210, 107477.	1.3	1
110	The Vibrio cholerae SpeG Spermidine/Spermine N-Acetyltransferase Allosteric Loop and $\hat{l}^26-\hat{l}^27$ Structural Elements Are Critical for Kinetic Activity. Frontiers in Molecular Biosciences, 2021, 8, 645768.	1.6	1
111	Overview of the Pipeline for Structural and Functional Characterization of Macrophage Proteins at the University of Queensland. Methods in Molecular Biology, 2008, 426, 577-587.	0.4	1
112	Nuclear Protein Import., 2005,, 137-160.		1
113	Purification, crystallization and preliminary X-ray diffraction analysis of theN-acetyltransferase SAV0826 fromStaphylococcus aureus. Acta Crystallographica Section F, Structural Biology Communications, 2014, 70, 211-214.	0.4	O
114	Molecular Characterization of a Beak and Feather Disease Virus Genome from a Purple Crowned Lorikeet (Glossopsitta porphyrocephala). Genome Announcements, 2016, 4, .	0.8	O
115	Complete mitochondrial genome sequence of an Australian little penguin (Eudyptula minor) Tj ETQq1 1 0.784314	l rgBT /0	Overlock 10 Tf
116	Nuclear Import Properties of the Sex-Determining Factor SRY., 0,, 83-98.		0